

DNA Seq Search Summary

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 14, 2003, 01:23:19 ; Search time 13662 Seconds
(without alignments)
17851.084 Million cell updates/sec

Title: US-09-775-938A-37
Perfect score: 8380
Sequence: 1 gcaccgttggaacgttatgg.....arargggcaaaaaaaaaaan 8380

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*

28: em_un:*
 29: em_vi:*
 30: em_htg_hum:*
 31: em_htg_inv:*
 32: em_htg_other:*
 33: em_htg_mus:*
 34: em_htg_pln:*
 35: em_htg_rod:*
 36: em_htg_mam:*
 37: em_htg_vrt:*
 38: em_sy:*
 39: em_htgo_hum:*
 40: em_htgo_mus:*
 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%		Query		DB		ID	Description
	No.	Score	Match	Length				
	1	8196.8	97.8	8380	6	AX083257	AX083257	Sequence
	2	236.2	2.8	13614	1	BSPKSH	Z14098	B.subtilis
	3	236.2	2.8	33615	1	BSU11039	U11039	Bacillus su
	4	236.2	2.8	233780	1	BSUB0010	Z99113	Bacillus su
c	5	199.4	2.4	11856	1	AE004344	AE004344	Vibrio ch
	6	174.8	2.1	1803	1	PAGORG	X54201	P. aerugino
	7	174.8	2.1	10541	1	AE004629	AE004629	Pseudomon
c	8	169	2.0	342800	1	AP003598	AP003598	Nostoc sp
	9	167.4	2.0	1805	1	A7120GOR	X89712	Anabaena PC
	10	160.2	1.9	7178	1	MXA6977	AJ006977	Myxococcu
c	11	158.4	1.9	11714	1	AE009538	AE009538	Brucella
	12	139.4	1.7	7735	1	BSPOLKET	Z35133	B.subtilis
	13	132.4	1.6	2029	6	A43677	A43677	Sequence 2
	14	132.4	1.6	2063	8	PSGLRED	X60373	P.sativum m
	15	129.2	1.5	2211	8	NCGMGRE	X76293	N.tabacum g
	16	128.4	1.5	1995	8	AF019907	AF019907	Vitis vin
	17	126.8	1.5	6000	6	AX083249	AX083249	Sequence
	18	126.4	1.5	5482	1	BCU19883	U19883	Burkholderi
	19	125.4	1.5	2081	8	SOYGLUTR	L11632	Soybean glu
	20	125.4	1.5	2672	6	AX083254	AX083254	Sequence
	21	124.6	1.5	4684	6	AX416809	AX416809	Sequence
c	22	124.2	1.5	348527	1	AP003360	AP003360	Staphyloc
	23	123.4	1.5	270050	1	AL591977	AL591977	Listeria
	24	123	1.5	2042	8	AF109694	AF109694	Brassica
c	25	122.6	1.5	290150	1	AP004824	AP004824	Staphyloc
	26	122	1.5	1968	8	AF349449	AF349449	Brassica
	27	121.2	1.4	1993	8	ATHGR	D14049	Arabidopsis
	28	121.2	1.4	2045	8	AY054677	AY054677	Arabidops
c	29	121	1.4	52276	1	AE014141	AE014141	Streptoco
c	30	116.6	1.4	12575	1	AE009977	AE009977	Streptoco
c	31	116.6	1.4	12578	1	AE006497	AE006497	Streptoco
c	32	114.6	1.4	224650	1	AL596164	AL596164	Listeria
c	33	114.6	1.4	349980	6	AX417038	AX417038	Sequence

OM nucleic - nucleic search, using sw model

Run on: January 14, 2003, 01:20:14 ; Search time 1017 Seconds
(without alignments)
18556.289 Million cell updates/sec

Title: US-09-775-938A-37
Perfect score: 8380
Sequence: 1 gcaccgttggaacgttatgg.....arargggcaaaaaaaaaaaaaan 8380

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_101002:*

- 1: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
- 2: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
- 3: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
- 4: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
- 5: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
- 6: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
- 7: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
- 8: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
- 9: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
- 10: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
- 11: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
- 12: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
- 13: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
- 14: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
- 15: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
- 16: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
- 17: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
- 18: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
- 19: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
- 20: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
- 21: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
- 22: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
- 23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
- 24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				ID	Description
	No.	Score	Match	Length	DB			
	1	8196.8	97.8	8380	24	AAD29007	Bugula neritina co	
	2	5427.8	64.8	5814	24	AAD29008	B. neritina cosmid	
	3	160.2	1.9	7178	21	AAA59145	DNA encoding a pep	
	4	132.4	1.6	2029	16	AAQ87912	Glutathione-reduct	
	5	126.8	1.5	6000	24	AAD28999	Bugula neritina PK	
	6	125.4	1.5	2672	24	AAD29004	Bugula neritina co	
	7	124.6	1.5	4684	24	ABQ70987	Listeria monocytog	
c	8	116.6	1.4	714	24	ABN68868	Streptococcus poly	
	9	110.6	1.3	31063	22	AAF28533	Genomic fragment #	
c	10	110.2	1.3	3803	22	AAH54197	S. epidermidis gen	
c	11	109.4	1.3	4017	22	AAH54064	S. epidermidis gen	
	12	108.8	1.3	1359	24	ABN66981	Streptococcus poly	
	13	108.2	1.3	7147	19	AAV52156	Streptococcus pneu	
c	14	106.6	1.3	726	24	ABN93298	Staphylococcus epi	
c	15	106.6	1.3	771	24	ABN68867	Streptococcus poly	
	16	106.6	1.3	2155561	24	ABN71527	Streptococcus poly	
c	17	105.4	1.3	2944528	24	ABA03041	Listeria monocytog	
c	18	105.2	1.3	714	24	ABN71086	Streptococcus poly	
	19	105	1.3	5686	24	AAD29001	Bugula neritina co	
c	20	104	1.2	717	22	AAH53866	S. epidermidis ope	
c	21	104	1.2	717	22	AAH53879	S. epidermidis ope	
	22	102.2	1.2	1680	24	ABQ70472	Listeria monocytog	
	23	101.8	1.2	7989	20	AAX13206	Enterococcus faeca	
c	24	98.2	1.2	717	21	AAA95485	E. coli essential	
c	25	98.2	1.2	717	21	AAA88712	E. coli FUN essent	
c	26	98.2	1.2	717	22	AAH81406	Escherichia coli p	
	27	96.6	1.2	1347	24	ABN66980	Streptococcus poly	
	28	94.2	1.1	1350	21	AAA05870	Group B Streptococ	
	29	94.2	1.1	1350	22	AAS07028	DNA encoding Group	
	30	92.8	1.1	1368	22	AAF94383	Haemophilus influe	
	31	92.8	1.1	1368	24	ABK64947	DNA encoding Haemo	
c	32	86.6	1.0	654	22	AAS07042	DNA encoding Group	
	33	86.6	1.0	2206	22	AAS41779	Genomic sequence #	
	34	86.6	1.0	2206	22	AAS41823	Genomic sequence #	
	35	86.6	1.0	2206	22	AAS41872	Genomic sequence #	
	36	86.6	1.0	2206	22	AAL02886	Human reproductive	
	37	86.6	1.0	2206	22	AAL02916	Human reproductive	
	38	86.6	1.0	2206	22	AAK69626	Human immune/haema	
	39	86.6	1.0	2206	22	AAK85452	Human immune/haema	
	40	86.6	1.0	2206	22	AAK85502	Human immune/haema	
	41	82.6	1.0	6373	21	AAA51639	pGM795 containing	
	42	81.8	1.0	5890	21	AAA51637	Plasmid pGM769 con	
	43	81.6	1.0	862	24	AAD29379	Beta-lactamase gen	
	44	81.6	1.0	4811	23	AAS92120	DNA encoding novel	
	45	81.6	1.0	6062	13	AAQ20765	pAD-CMV19. AAQ20	

ALIGNMENTS

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OM nucleic - nucleic search, using sw model

Run on: January 14, 2003, 02:32:09 ; Search time 166 Seconds
(without alignments)
15481.634 Million cell updates/sec

Title: US-09-775-938A-37
Perfect score: 8380
Sequence: 1 gcaccgttggaacgttatgg.....arargggcaaaaaaaaaa 8380

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query				Description
	No.	Score	Match	Length	DB	ID			
	1	108.2	1.3	7147	4	US-08-961-527-23			Sequence 23, Appl
c	2	106.6	1.3	726	4	US-09-134-001C-2761			Sequence 2761, Ap
c	3	80	1.0	1106	1	US-08-041-648-4			Sequence 4, Appli
c	4	80	1.0	1106	1	US-08-041-648-6			Sequence 6, Appli
c	5	80	1.0	1106	1	US-08-041-648-8			Sequence 8, Appli
	6	80	1.0	1163	4	US-09-025-769B-284			Sequence 284, App
c	7	80	1.0	1289	4	US-09-025-769B-361			Sequence 361, App
	8	80	1.0	1947	4	US-09-025-769B-264			Sequence 264, App
	9	80	1.0	2422	1	US-07-867-106-5			Sequence 5, Appli
c	10	80	1.0	2728	4	US-09-025-769B-299			Sequence 299, App
c	11	80	1.0	2755	2	US-07-916-098A-7			Sequence 7, Appli
	12	80	1.0	2927	2	US-08-941-647A-1			Sequence 1, Appli

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OM nucleic - nucleic search, using sw model

Run on: January 14, 2003, 02:35:14 ; Search time 230 Seconds
(without alignments)
16035.070 Million cell updates/sec

Title: US-09-775-938A-37
Perfect score: 8380
Sequence: 1 gcaccgttggaacgttatgg.....arargggcaaaaaaaaaa 8380

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 389086 seqs, 220051671 residues

Total number of hits satisfying chosen parameters: 778172

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	8196.8	97.8	8380	10	US-09-775-938A-37	Sequence 37, Appl
2	126.8	1.5	6000	10	US-09-775-938A-29	Sequence 29, Appl
3	125.4	1.5	2672	10	US-09-775-938A-34	Sequence 34, Appl
4	121.2	1.4	1698	9	US-09-938-842A-1742	Sequence 1742, Ap

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OM nucleic - nucleic search, using sw model

Run on: January 14, 2003, 02:29:49 ; Search time 6839 Seconds
(without alignments)
19844.740 Million cell updates/sec

Title: US-09-775-938A-37
Perfect score: 8380
Sequence: 1 gcaccgttggaacgttatgg.....arargggcaaaaaaaaaaan 8380

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estmu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_htc:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_htc:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: gb_gss:*
- 18: em_gss_hum:*
- 19: em_gss_inv:*
- 20: em_gss_pln:*
- 21: em_gss_vrt:*
- 22: em_gss_fun:*
- 23: em_gss_mam:*
- 24: em_gss_mus:*
- 25: em_gss_other:*
- 26: em_gss_pro:*
- 27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match Length	DB	ID	Description
	1	114.6	1.4	775	13	BI925816
	2	114	1.4	612	13	BJ481803
c	3	109.4	1.3	2553	17	BH771010
	4	104.2	1.2	694	13	BI923097
	5	103.4	1.2	756	13	BI926373
	6	99.8	1.2	626	12	BF597723
	7	99.8	1.2	631	10	AW201729
	8	99.2	1.2	660	10	AW692989
	9	98.6	1.2	720	10	BE038718
	10	98.2	1.2	543	12	BE800059
	11	97	1.2	593	10	AW759724
	12	95.8	1.1	588	13	BI921333
	13	94.4	1.1	581	10	AV937628
	14	93.6	1.1	509	14	BQ490169
c	15	93.2	1.1	888	13	BI684711
	16	92.6	1.1	713	10	BE435454
	17	88.8	1.1	935	12	BG838279
c	18	86.6	1.0	535	17	AZ049308
c	19	86.6	1.0	773	13	BI686035
	20	86.2	1.0	1931	11	AY103791
	21	86	1.0	473	13	BM093562
	22	85.4	1.0	707	9	AU056093
c	23	83.6	1.0	911	13	BG923556
c	24	83.2	1.0	832	13	BG923768
c	25	83.2	1.0	855	13	BI664231
	26	82	1.0	490	13	BM323249
	27	82	1.0	683	14	BQ283215
	28	80	1.0	444	14	BQ469551
	29	80	1.0	499	10	AV612734
c	30	80	1.0	575	17	AZ918759
c	31	80	1.0	604	17	AG002706
c	32	80	1.0	711	17	AG010947
c	33	80	1.0	754	13	BG920379
	34	80	1.0	780	14	BQ825693
	35	80	1.0	841	9	AL042026
c	36	79.8	1.0	803	13	BI149831
	37	79.6	0.9	583	10	BE498405
	38	79.6	0.9	647	17	AG008943
	39	79.2	0.9	608	13	BM325129
c	40	79.2	0.9	872	13	BI855537
	41	78.8	0.9	549	13	BI944287
	42	78.8	0.9	618	14	BQ820772
	43	78	0.9	415	13	BI972926
c	44	78	0.9	801	10	BE569687
	45	77.8	0.9	691	14	BU002083

ALIGNMENTS